



SEQUENCE LISTING

<110> BASLER, Konrad
BRUNNER, Erich
FROESCH, Barbara
KRAMPS, Thomas
PETER, Oliver

<120> ESSENTIAL DOWNSTREAM COMPONENT OF THE WINGLESS SIGNALING PATHWAY
AND THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED THEREON

<130> Q77377

<140> 10/664,859
<141> 2003-09-22

<150> US 09/915,543
<151> 2001-07-27

<150> 60/221,502
<151> 2000-07-28

<160> 25

<170> PatentIn version 3.3

<210> 1
<211> 6909
<212> DNA
<213> Drosophila lgs

<220>
<221> exon
<222> (468) .. (632)

<220>
<221> exon
<222> (691) .. (981)

<220>
<221> exon
<222> (1456) .. (1665)

<220>
<221> exon
<222> (2394) .. (4397)

<220>
<221> exon

<222> (4679) .. (4870)

<220>

<221> exon

<222> (4927) .. (6456)

<400> 1

acgagtgctt ctcttattat gcgagctggt tattccaaag tatgttcgca attttcgact 60

cctgctaaca taacgcacgg ttaaagcagg aacatttggg cctataagcc caaaatttca 120

ttagcttaat acgatgctcc gaagtgttat tgcatttgca catatacata aaattgtgac 180

atagaatagg agaattccac atacaaatac aaaaatacaa aatcctccag taaaatttaa 240

aacgatatcg tgtttttgctt cgcgtatctc acgtgagatg taatcgcgat catatgagtg 300

gtgagtgctt gcgtgcagtt cctgggtctaa atatgcttaa ttgcgttcgc cgacttcaaa 360

agcaataaaa cgatggattt taattgctac ttgagcaatt agccacacaa gggatcttgg 420

gaaggtcgat ttgaaggaat tcgatttcta ggatgctctc gacaaca atg ccc cgc 476
Met Pro Arg
1

agt cca acc caa caa cag ccg caa cca aac tcc gat gcc tcc tca aca 524
Ser Pro Thr Gln Gln Gln Pro Gln Pro Asn Ser Asp Ala Ser Ser Thr
5 10 15

agt gca tct gga tca aat cct gga gca gcg atc gga aat ggg gac tcg 572
Ser Ala Ser Gly Ser Asn Pro Gly Ala Ala Ile Gly Asn Gly Asp Ser
20 25 30 35

gcg gcg agc aga agt tct ccg aag acc ctt aat agc gaa ccc ttt tct 620
Ala Ala Ser Arg Ser Ser Pro Lys Thr Leu Asn Ser Glu Pro Phe Ser
40 45 50

act ttg tcg ccg ggtaagactt gtattgattt ctctttgtcc ggaattataa 672
Thr Leu Ser Pro
55

caactttctg tgttttcca gat caa ata aaa ttg acg cca gaa gaa ggc act 723
Asp Gln Ile Lys Leu Thr Pro Glu Glu Gly Thr
60 65

gag aaa agc gga cta tca act agt gat aaa gct gcc act gga gga gcc 771
Glu Lys Ser Gly Leu Ser Thr Ser Asp Lys Ala Ala Thr Gly Gly Ala
70 75 80

cca ggc agt gga aat aat ctg ccc gag gga caa act atg cta agg cag 819

Pro	Gly	Ser	Gly	Asn	Asn	Leu	Pro	Glu	Gly	Gln	Thr	Met	Leu	Arg	Gln		
		85					90					95					
aac	tct	acg	agc	aca	atc	aac	tcg	tgc	cta	gtc	gct	tct	cca	caa	aac		867
Asn	Ser	Thr	Ser	Thr	Ile	Asn	Ser	Cys	Leu	Val	Ala	Ser	Pro	Gln	Asn		
	100					105					110						
tcc	agt	gaa	cac	tcg	aat	agc	agc	aat	gtg	tct	gct	aca	gtg	ggc	ctt		915
Ser	Ser	Glu	His	Ser	Asn	Ser	Ser	Asn	Val	Ser	Ala	Thr	Val	Gly	Leu		
115					120					125					130		
act	cag	atg	gta	gat	tgt	gac	gag	caa	tcg	aag	aaa	aac	aaa	tgt	agt		963
Thr	Gln	Met	Val	Asp	Cys	Asp	Glu	Gln	Ser	Lys	Lys	Asn	Lys	Cys	Ser		
				135					140					145			
gtg	aag	gac	gag	gaa	gct	ggtaagactg	ccctacaaat	ggtttaaaat									1011
Val	Lys	Asp	Glu	Glu	Ala												
			150														
tttaaaatgt	attggcggttc	acctttgtta	atcatttaat	tgttttttttt	ttgctataact												1071
tacaatttta	gttttaaaact	tgtaaacttg	actaaaactc	gcgaagctcg	gatcaaaaca												1131
gacattttct	tggaaccgta	attaagctca	taaaaatatt	aattcatctt	gatggaatgc												1191
atatcataga	tgtactcaaa	catctcaaga	aagacctcaa	attggatcaa	ctaattagtt												1251
tgagaaaaaa	ttgctgtact	tttaagaata	tattaattta	aaaatttgct	gagtgaaatg												1311
atataatagt	cacaataatt	tttagttaaa	ctgctaaagc	attttgaata	gccgtgctac												1371
gcagatgcta	ctagacgcgg	tgtaaaagct	aattttttatt	taaaagctgt	cctaatatctc												1431
cataaccatt	aatgtcccat	ttca	gaa	ata	agt	tct	aat	aaa	gca	aaa	ggt						1482
			Glu	Ile	Ser	Ser	Asn	Lys	Ala	Lys	Gly						
							155				160						
caa	gca	gct	ggt	ggc	ggc	tgc	gaa	aca	ggt	tct	aca	tcc	agt	ttg	act		1530
Gln	Ala	Ala	Gly	Gly	Gly	Cys	Glu	Thr	Gly	Ser	Thr	Ser	Ser	Leu	Thr		
			165					170					175				
gtc	aag	gaa	gaa	ccc	acc	gat	gtc	tta	ggc	agt	tta	gta	aat	atg	aaa		1578
Val	Lys	Glu	Glu	Pro	Thr	Asp	Val	Leu	Gly	Ser	Leu	Val	Asn	Met	Lys		
		180					185					190					
aaa	gaa	gaa	aga	gaa	aat	cat	tcg	cca	acg	atg	tcc	cct	gtt	ggt	ttt		1626
Lys	Glu	Glu	Arg	Glu	Asn	His	Ser	Pro	Thr	Met	Ser	Pro	Val	Gly	Phe		
	195					200					205						
ggt	tca	att	ggt	aat	gca	cag	gac	aac	tcc	gct	aca	ccg	ggtaagtttt				1675

Gly Ser Ile Gly Asn Ala Gln Asp Asn Ser Ala Thr Pro	
210	215 220
aagagatcca tataaagcaa ataacaagaa ttaatgtcag ttaccaattt tatttgatag	1735
tcaaagaact actatagcga tatctcctgc cttttaattt tattttaatt aggaaatacg	1795
aatattttcta atttgtaaaa taaaattgat taattaacta gaatttaaaa accttttgaa	1855
ttaggacata cccttccaaa aatcagtaat cattgggaac gagagtgtgg tcccgaagga	1915
gactactata aaaccttttg agctatctga tactgcacgc tactaaaaat gattagttta	1975
ggaaaatggg tgtaattttg taggaagttt tcatttttaga agaaatgtga ttattttatt	2035
aaacccttc aagcggaact acatttgttc tacgatattt tggaaaaaca aatgggtaag	2095
ttggaaagtg cctataaaac agaattccac ggtttcaaact actaaccagg tttttgattt	2155
aattttgatt aatgagaaa ttatcacact tcagttaaaa tgtttaattc gattaaggtc	2215
ggacaatcac agcagatttc catttttgcg tgtatatata gaagtcgcct tcacactctt	2275
ctggcgcgct tcaccactac gtggagttcc gcccgcagtg atttatatag atgatttacg	2335
agttatttaa ttttttatgg tgtatttttaa taaatatctt atttattcat tttacata	2393
gtt aaa att gaa aga att tca aac gac agt acc acg gaa aaa aaa gga	2441
Val Lys Ile Glu Arg Ile Ser Asn Asp Ser Thr Thr Glu Lys Lys Gly	
225 230 235	
tcg tcc ttg aca atg aat aat gac gaa atg agc atg gaa ggc tgc aat	2489
Ser Ser Leu Thr Met Asn Asn Asp Glu Met Ser Met Glu Gly Cys Asn	
240 245 250	
cag ttg aat ccc gat ttt atc aat gaa tct tta aat aat cct gca att	2537
Gln Leu Asn Pro Asp Phe Ile Asn Glu Ser Leu Asn Asn Pro Ala Ile	
255 260 265 270	
tcg agc ata tta gta agc gga gta gga cca ata ccc gga atc gga gtt	2585
Ser Ser Ile Leu Val Ser Gly Val Gly Pro Ile Pro Gly Ile Gly Val	
275 280 285	
gga gcg ggg acg gga aat tta ttg act gcc aac gcc aat gga atc tcc	2633
Gly Ala Gly Thr Gly Asn Leu Leu Thr Ala Asn Ala Asn Gly Ile Ser	
290 295 300	
tcg ggt agc agt aat tgt ttg gat tac atg caa cag caa aat cac ata	2681
Ser Gly Ser Ser Asn Cys Leu Asp Tyr Met Gln Gln Gln Asn His Ile	
305 310 315	

ttc	gtg	ttt	tca	act	cag	ctg	gcc	aac	aaa	ggg	gcc	gaa	tca	gtt	tta	2729
Phe	Val	Phe	Ser	Thr	Gln	Leu	Ala	Asn	Lys	Gly	Ala	Glu	Ser	Val	Leu	
	320					325					330					
agc	ggt	caa	ttt	caa	act	att	att	gcg	tat	cac	tgc	act	cag	cct	gct	2777
Ser	Gly	Gln	Phe	Gln	Thr	Ile	Ile	Ala	Tyr	His	Cys	Thr	Gln	Pro	Ala	
335					340					345					350	
aca	aaa	agc	ttc	ctg	gaa	gac	ttt	ttt	atg	aaa	aac	cct	tta	aag	att	2825
Thr	Lys	Ser	Phe	Leu	Glu	Asp	Phe	Phe	Met	Lys	Asn	Pro	Leu	Lys	Ile	
				355					360					365		
aac	aag	tta	cag	cgg	cac	aat	tcc	gtc	ggt	atg	cca	tgg	ata	ggc	atg	2873
Asn	Lys	Leu	Gln	Arg	His	Asn	Ser	Val	Gly	Met	Pro	Trp	Ile	Gly	Met	
			370					375					380			
ggg	cag	gtt	gga	cta	act	cct	cct	aat	cct	gta	gcc	aaa	ata	aca	caa	2921
Gly	Gln	Val	Gly	Leu	Thr	Pro	Pro	Asn	Pro	Val	Ala	Lys	Ile	Thr	Gln	
		385					390					395				
cag	cag	cca	cat	aca	aag	acc	gta	ggc	cta	ttg	aaa	ccc	caa	ttc	aat	2969
Gln	Gln	Pro	His	Thr	Lys	Thr	Val	Gly	Leu	Leu	Lys	Pro	Gln	Phe	Asn	
	400					405					410					
caa	cat	gaa	aac	agc	aaa	cgt	agt	act	gta	agc	gcg	cct	agc	aac	tct	3017
Gln	His	Glu	Asn	Ser	Lys	Arg	Ser	Thr	Val	Ser	Ala	Pro	Ser	Asn	Ser	
415					420					425					430	
ttt	gtc	gac	cag	tct	gat	cct	atg	ggc	aac	gaa	act	gaa	ttg	atg	tgc	3065
Phe	Val	Asp	Gln	Ser	Asp	Pro	Met	Gly	Asn	Glu	Thr	Glu	Leu	Met	Cys	
				435					440					445		
tgg	gaa	ggc	gga	tcc	tca	aac	acc	agt	agg	tct	gga	caa	aac	tca	cga	3113
Trp	Glu	Gly	Gly	Ser	Ser	Asn	Thr	Ser	Arg	Ser	Gly	Gln	Asn	Ser	Arg	
			450					455					460			
aat	cat	gta	gac	agt	atc	agt	aca	tcc	agc	gag	tca	cag	gca	ata	aag	3161
Asn	His	Val	Asp	Ser	Ile	Ser	Thr	Ser	Ser	Glu	Ser	Gln	Ala	Ile	Lys	
		465					470					475				
ata	ctg	gaa	gca	gct	ggc	gtt	gat	ttg	gga	cag	gtc	aca	aaa	gga	agc	3209
Ile	Leu	Glu	Ala	Ala	Gly	Val	Asp	Leu	Gly	Gln	Val	Thr	Lys	Gly	Ser	
	480					485					490					
gat	cct	ggc	ctg	aca	act	gaa	aac	aac	att	gta	tca	ctg	caa	gga	gtt	3257
Asp	Pro	Gly	Leu	Thr	Thr	Glu	Asn	Asn	Ile	Val	Ser	Leu	Gln	Gly	Val	
495					500					505					510	
aag	gtt	cca	gac	gaa	aac	ctt	aca	cca	caa	cag	cgg	caa	cat	cgg	gaa	3305

Lys	Val	Pro	Asp	Glu	Asn	Leu	Thr	Pro	Gln	Gln	Arg	Gln	His	Arg	Glu	
				515					520					525		
gaa	cag	ttg	gca	aaa	ata	aaa	aaa	atg	aat	caa	ttt	ctt	ttt	cct	gaa	3353
Glu	Gln	Leu	Ala	Lys	Ile	Lys	Lys	Met	Asn	Gln	Phe	Leu	Phe	Pro	Glu	
			530					535					540			
aat	gag	aat	tca	gta	gga	gct	aat	gta	agc	tca	cag	ata	aca	aaa	att	3401
Asn	Glu	Asn	Ser	Val	Gly	Ala	Asn	Val	Ser	Ser	Gln	Ile	Thr	Lys	Ile	
		545					550					555				
cca	gga	gat	tta	atg	atg	ggg	atg	tcg	ggc	ggc	gga	ggc	gga	tct	att	3449
Pro	Gly	Asp	Leu	Met	Met	Gly	Met	Ser	Gly	Gly	Gly	Gly	Gly	Ser	Ile	
	560					565					570					
ata	aat	ccg	acg	atg	cga	caa	ctg	cat	atg	cca	ggc	aac	gcc	aaa	tcg	3497
Ile	Asn	Pro	Thr	Met	Arg	Gln	Leu	His	Met	Pro	Gly	Asn	Ala	Lys	Ser	
575					580					585					590	
gag	ctc	tta	tcg	gcg	aca	agt	tca	gga	ctt	tcg	gaa	gat	gta	atg	cat	3545
Glu	Leu	Leu	Ser	Ala	Thr	Ser	Ser	Gly	Leu	Ser	Glu	Asp	Val	Met	His	
				595					600					605		
cca	ggg	gat	gtt	ata	tca	gat	atg	ggc	gcc	gta	ata	gga	tgt	aat	aat	3593
Pro	Gly	Asp	Val	Ile	Ser	Asp	Met	Gly	Ala	Val	Ile	Gly	Cys	Asn	Asn	
			610					615					620			
aat	caa	aaa	acc	agt	gtg	caa	tgt	gga	tct	gga	gta	ggc	gtt	gtc	act	3641
Asn	Gln	Lys	Thr	Ser	Val	Gln	Cys	Gly	Ser	Gly	Val	Gly	Val	Val	Thr	
		625					630					635				
gga	aca	act	gca	gct	gga	gta	aat	gtc	aat	atg	cat	tgc	tca	agc	tcc	3689
Gly	Thr	Thr	Ala	Ala	Gly	Val	Asn	Val	Asn	Met	His	Cys	Ser	Ser	Ser	
	640					645					650					
ggc	gcc	ccg	aat	ggc	aat	atg	atg	gga	agc	tct	acg	gat	atg	cta	gcc	3737
Gly	Ala	Pro	Asn	Gly	Asn	Met	Met	Gly	Ser	Ser	Thr	Asp	Met	Leu	Ala	
655					660					665					670	
tcg	ttt	ggc	aac	aca	agc	tgc	aac	gtc	atc	gga	acg	gcc	cca	gat	atg	3785
Ser	Phe	Gly	Asn	Thr	Ser	Cys	Asn	Val	Ile	Gly	Thr	Ala	Pro	Asp	Met	
				675					680					685		
tct	aag	gaa	gtt	tta	aat	caa	gat	agc	cga	acc	cat	tca	cat	caa	ggg	3833
Ser	Lys	Glu	Val	Leu	Asn	Gln	Asp	Ser	Arg	Thr	His	Ser	His	Gln	Gly	
			690					695					700			
gga	gtt	gct	caa	atg	gag	tgg	tcg	aag	att	caa	cat	caa	ttt	ttc	gaa	3881
Gly	Val	Ala	Gln	Met	Glu	Trp	Ser	Lys	Ile	Gln	His	Gln	Phe	Phe	Glu	
		705					710					715				

gaa cgc ctc aag ggg ggc aag ccc aga caa gtc act gga act gta gta	3929
Glu Arg Leu Lys Gly Gly Lys Pro Arg Gln Val Thr Gly Thr Val Val	
720 725 730	
cca caa cag caa acc cct tct gga tct ggt gga aac tcg tta aac aac	3977
Pro Gln Gln Gln Thr Pro Ser Gly Ser Gly Gly Asn Ser Leu Asn Asn	
735 740 745 750	
cag gtg cga ccc ctg caa ggt cca cct cct cct tac cac tcc atc cag	4025
Gln Val Arg Pro Leu Gln Gly Pro Pro Pro Pro Tyr His Ser Ile Gln	
755 760 765	
aga tct gcg tca gta cca ata gcc act caa tcg ccc aat ccc tcg agt	4073
Arg Ser Ala Ser Val Pro Ile Ala Thr Gln Ser Pro Asn Pro Ser Ser	
770 775 780	
cca aac aat cta tct ctc ccg tca ccg cgg aca acc gca gca gtc atg	4121
Pro Asn Asn Leu Ser Leu Pro Ser Pro Arg Thr Thr Ala Ala Val Met	
785 790 795	
gga ttg ccg acc aac tct cct agc atg gat gga aca gga tca tta tct	4169
Gly Leu Pro Thr Asn Ser Pro Ser Met Asp Gly Thr Gly Ser Leu Ser	
800 805 810	
gga tct gtt ccg caa gct aat act tcg acg gtt cag gca ggc aca aca	4217
Gly Ser Val Pro Gln Ala Asn Thr Ser Thr Val Gln Ala Gly Thr Thr	
815 820 825 830	
aca gtg ctc tca gca aac aag aac tgt ttt cag gca gac acc cca tcg	4265
Thr Val Leu Ser Ala Asn Lys Asn Cys Phe Gln Ala Asp Thr Pro Ser	
835 840 845	
ccg tca aat caa aat cgt agt aga aat acc gga tcg tca agc gtt ctt	4313
Pro Ser Asn Gln Asn Arg Ser Arg Asn Thr Gly Ser Ser Ser Val Leu	
850 855 860	
acg cat aac tta agc agc aac cca agt acc ccc tta tct cat cta tcc	4361
Thr His Asn Leu Ser Ser Asn Pro Ser Thr Pro Leu Ser His Leu Ser	
865 870 875	
cca aag gaa ttt gag tct ttc ggt cag tcc tct gct ggtatggttat	4407
Pro Lys Glu Phe Glu Ser Phe Gly Gln Ser Ser Ala	
880 885 890	
atttgtttaa ttttttttaa gacaaatcaa atatgaattg cgттаатаат aagttatata	4467
ttacataact cgгaaatttg atagaaaaaa tcaggaatag aaaaaataaa ttatttttccg	4527
gaccgccccat ccattttcttg aatccaattt ctggagtgat tgttagagat aatctactat	4587

taaaattaaa cacgaaaatt catatccggtt aattgaaaat cactattggtt taataagaaa	4647
ttaaaaatat gtttattata atatttctac a ggt gat aac atg aaa agt agg	4699
Gly Asp Asn Met Lys Ser Arg	895
cga cca agc cca cag ggt cag cgg tca cca gta aat agt cta ata gag	4747
Arg Pro Ser Pro Gln Gly Gln Arg Ser Pro Val Asn Ser Leu Ile Glu	900 905 910
gca aat aaa gat gta cga ttt gct gca tcc agt cct ggt ttt aac ccg	4795
Ala Asn Lys Asp Val Arg Phe Ala Ala Ser Ser Pro Gly Phe Asn Pro	915 920 925
cat cca cat atg caa agc aat tca aat tca gca tta aac gcc tat aaa	4843
His Pro His Met Gln Ser Asn Ser Asn Ser Ala Leu Asn Ala Tyr Lys	930 935 940 945
atg ggc tct acc aat ata cag atg gag gtaaataattt aaataatttta	4890
Met Gly Ser Thr Asn Ile Gln Met Glu	950
tttaacgttt ttgtgttaat ttatcttctt tttcag cgt caa gca tca gcg caa	4944
Arg Gln Ala Ser Ala Gln	955 960
ggt gga tcc gta caa ttt agt cgg cgc tcc gat aat att ccg cta aat	4992
Gly Gly Ser Val Gln Phe Ser Arg Arg Ser Asp Asn Ile Pro Leu Asn	965 970 975
ccc aat agt ggc aat cgg ccg cca cca aac aag atg acc caa aac ttc	5040
Pro Asn Ser Gly Asn Arg Pro Pro Pro Asn Lys Met Thr Gln Asn Phe	980 985 990
gat cca atc tct tct ttg gca caa atg tcc caa caa cta aca agt tgc	5088
Asp Pro Ile Ser Ser Leu Ala Gln Met Ser Gln Gln Leu Thr Ser Cys	995 1000 1005
gtg tcc agc atg ggt agt cca gcc gga act ggt ggt atg acg atg	5133
Val Ser Ser Met Gly Ser Pro Ala Gly Thr Gly Gly Met Thr Met	1010 1015 1020
atg ggg ggt ccg gga ccg tcc gac atc aat att gag cat gga ata	5178
Met Gly Gly Pro Gly Pro Ser Asp Ile Asn Ile Glu His Gly Ile	1025 1030 1035
att tcg gga cta gat gga tca gga ata gat acc ata aat caa aat	5223
Ile Ser Gly Leu Asp Gly Ser Gly Ile Asp Thr Ile Asn Gln Asn	1040 1045 1050

aac	tgt	cat	tca	atg	aat	gtc	gta	atg	aac	tca	atg	ggc	ccc	cga	5268
Asn	Cys	His	Ser	Met	Asn	Val	Val	Met	Asn	Ser	Met	Gly	Pro	Arg	
	1055					1060					1065				
atg	ctg	aat	cct	aaa	atg	tgc	gta	gca	ggc	ggc	cca	aat	gga	ccg	5313
Met	Leu	Asn	Pro	Lys	Met	Cys	Val	Ala	Gly	Gly	Pro	Asn	Gly	Pro	
	1070					1075					1080				
cct	ggc	ttt	aat	cct	aat	tcc	ccc	aat	ggc	gga	tta	aga	gag	aat	5358
Pro	Gly	Phe	Asn	Pro	Asn	Ser	Pro	Asn	Gly	Gly	Leu	Arg	Glu	Asn	
	1085					1090					1095				
tcc	ata	ggg	tct	ggc	tgt	ggc	tca	gca	aac	tct	tca	aac	ttt	caa	5403
Ser	Ile	Gly	Ser	Gly	Cys	Gly	Ser	Ala	Asn	Ser	Ser	Asn	Phe	Gln	
	1100					1105					1110				
ggg	gtt	gtt	cca	cct	ggc	gcc	aga	atg	atg	ggc	cga	atg	cca	gtc	5448
Gly	Val	Val	Pro	Pro	Gly	Ala	Arg	Met	Met	Gly	Arg	Met	Pro	Val	
	1115					1120					1125				
aat	ttt	ggc	tcg	aat	ttc	aat	ccg	aat	att	cag	gta	aag	gcg	agt	5493
Asn	Phe	Gly	Ser	Asn	Phe	Asn	Pro	Asn	Ile	Gln	Val	Lys	Ala	Ser	
	1130					1135					1140				
acc	cca	aac	acc	ata	caa	tac	atg	cca	gta	agg	gca	cag	aac	gcc	5538
Thr	Pro	Asn	Thr	Ile	Gln	Tyr	Met	Pro	Val	Arg	Ala	Gln	Asn	Ala	
	1145					1150					1155				
aac	aac	aat	aac	aac	aat	gga	gct	aat	aat	gtg	cga	atg	cca	cct	5583
Asn	Asn	Asn	Asn	Asn	Asn	Gly	Ala	Asn	Asn	Val	Arg	Met	Pro	Pro	
	1160					1165					1170				
agt	ctg	gaa	ttt	ttg	cag	agg	tac	gct	aac	cct	caa	atg	ggc	gct	5628
Ser	Leu	Glu	Phe	Leu	Gln	Arg	Tyr	Ala	Asn	Pro	Gln	Met	Gly	Ala	
	1175					1180					1185				
gta	ggc	aat	ggg	tcg	cca	ata	tgc	cca	cca	tca	gcc	agc	gac	ggc	5673
Val	Gly	Asn	Gly	Ser	Pro	Ile	Cys	Pro	Pro	Ser	Ala	Ser	Asp	Gly	
	1190					1195					1200				
act	cct	gga	atg	cca	gga	ttg	atg	gcg	gga	cca	gga	gcc	gga	ggc	5718
Thr	Pro	Gly	Met	Pro	Gly	Leu	Met	Ala	Gly	Pro	Gly	Ala	Gly	Gly	
	1205					1210					1215				
atg	cta	atg	aat	tct	tcc	gga	gag	caa	cac	cag	aac	aag	atc	aca	5763
Met	Leu	Met	Asn	Ser	Ser	Gly	Glu	Gln	His	Gln	Asn	Lys	Ile	Thr	
	1220					1225					1230				
aac	aat	cct	ggg	gca	agc	aat	ggc	att	aac	ttc	ttt	cag	aat	tgc	5808

Asn	Asn	Pro	Gly	Ala	Ser	Asn	Gly	Ile	Asn	Phe	Phe	Gln	Asn	Cys	
	1235					1240					1245				
aat	caa	atg	tct	att	gtt	gac	gaa	gag	ggt	gga	tta	ccc	ggc	cat	5853
Asn	Gln	Met	Ser	Ile	Val	Asp	Glu	Glu	Gly	Gly	Leu	Pro	Gly	His	
	1250					1255					1260				
gac	gga	tca	atg	aat	att	ggt	caa	cca	tct	atg	ata	agg	ggc	atg	5898
Asp	Gly	Ser	Met	Asn	Ile	Gly	Gln	Pro	Ser	Met	Ile	Arg	Gly	Met	
	1265					1270					1275				
cgt	cca	cat	gcc	atg	cgg	cca	aat	gta	atg	ggt	gcg	cgg	atg	cca	5943
Arg	Pro	His	Ala	Met	Arg	Pro	Asn	Val	Met	Gly	Ala	Arg	Met	Pro	
	1280					1285					1290				
ccc	gtt	aac	agg	caa	att	cag	ttt	gca	cag	tca	tcg	gat	ggc	att	5988
Pro	Val	Asn	Arg	Gln	Ile	Gln	Phe	Ala	Gln	Ser	Ser	Asp	Gly	Ile	
	1295					1300					1305				
gac	tgt	gtc	ggg	gat	ccg	tca	tca	ttt	ttc	act	aac	gct	tcc	tgc	6033
Asp	Cys	Val	Gly	Asp	Pro	Ser	Ser	Phe	Phe	Thr	Asn	Ala	Ser	Cys	
	1310					1315					1320				
aac	agc	gct	gga	cca	cac	atg	ttt	gga	tca	gca	caa	cag	gcc	aat	6078
Asn	Ser	Ala	Gly	Pro	His	Met	Phe	Gly	Ser	Ala	Gln	Gln	Ala	Asn	
	1325					1330					1335				
cag	cct	aag	aca	caa	cac	ata	aag	aac	ata	cct	agt	gga	atg	tgt	6123
Gln	Pro	Lys	Thr	Gln	His	Ile	Lys	Asn	Ile	Pro	Ser	Gly	Met	Cys	
	1340					1345					1350				
caa	aac	caa	tcg	gga	ctt	gca	gtg	gca	caa	ggg	cag	atc	caa	ctg	6168
Gln	Asn	Gln	Ser	Gly	Leu	Ala	Val	Ala	Gln	Gly	Gln	Ile	Gln	Leu	
	1355					1360					1365				
cat	ggg	caa	gga	cat	gcg	cag	ggt	cag	tct	tta	att	gga	cct	act	6213
His	Gly	Gln	Gly	His	Ala	Gln	Gly	Gln	Ser	Leu	Ile	Gly	Pro	Thr	
	1370					1375					1380				
aat	aat	aat	tta	atg	tca	act	gcc	gga	agt	gtc	agt	gct	act	aac	6258
Asn	Asn	Asn	Leu	Met	Ser	Thr	Ala	Gly	Ser	Val	Ser	Ala	Thr	Asn	
	1385					1390					1395				
ggt	gtc	tct	ggc	atc	aat	ttc	gta	ggt	ccc	tct	tct	acg	gac	ctg	6303
Gly	Val	Ser	Gly	Ile	Asn	Phe	Val	Gly	Pro	Ser	Ser	Thr	Asp	Leu	
	1400					1405					1410				
aag	tat	gcc	cag	caa	tat	cat	agt	ttt	cag	cag	cag	tta	tat	gct	6348
Lys	Tyr	Ala	Gln	Gln	Tyr	His	Ser	Phe	Gln	Gln	Gln	Leu	Tyr	Ala	
	1415					1420					1425				

acc aac acc aga agt caa caa caa cag cat atg cac cag cag cac	6393
Thr Asn Thr Arg Ser Gln Gln Gln Gln His Met His Gln Gln His	
1430 1435 1440	
cag agc aac atg ata aca atg ccg ccg aat tta tca cca aat cca	6438
Gln Ser Asn Met Ile Thr Met Pro Pro Asn Leu Ser Pro Asn Pro	
1445 1450 1455	
acg ttc ttt gtc aac aaa taaacttcta aattttttgcc gccctcgtca	6486
Thr Phe Phe Val Asn Lys	
1460	
tgtattgttt actagtctcc aaattaagac atgcatctct aaataagatt ttttgaagct	6546
tatttactta ggtgttttta caacggagaa aataaacttt tggatatgca aatgataacg	6606
ttggaaacaa cataattcat ttgcaacttt tagaagtcac gtcgaagtta aatgtagaat	6666
ctgtatttta acataatagg tcatctgtaa aaataattaa acatcgaaat tttagttatc	6726
agcagctatt ttctgttatt atttaatatg tgcgctgctc tctctgtgtt aaatgaaatt	6786
aaaatatata tataaatgta aaacgctatt gatatatatt gctctcaact gtattgtaat	6846
caatattaag agaactgtaa attcttccat ataaaggtaa tgaaaaaaaa aaaaaaaaaa	6906
aaa	6909

<210> 2
 <211> 28
 <212> PRT
 <213> Drosophila lgs

<400> 2

Ile Phe Val Phe Ser Thr Gln Leu Ala Asn Lys Gly Ala Glu Ser Val
1 5 10 15

Leu Ser Gly Gln Phe Gln Thr Ile Ile Ala Tyr His
20 25

<210> 3
 <211> 28
 <212> PRT
 <213> Human lgs/bcl9

<400> 3

Val Tyr Val Phe Ser Thr Glu Met Ala Asn Lys Ala Ala Glu Ala Val
1 5 10 15

Leu Lys Gly Gln Val Glu Thr Ile Val Ser Phe His
20 25

<210> 4

<211> 35

<212> PRT

<213> Drosophila lgs

<400> 4

Glu Asn Leu Thr Pro Gln Gln Arg Gln His Arg Glu Glu Gln Leu Ala
1 5 10 15

Lys Ile Lys Lys Met Asn Gln Phe Leu Phe Pro Glu Asn Glu Asn Ser
20 25 30

Val Gly Ala
35

<210> 5

<211> 35

<212> PRT

<213> Human lgs/bcl9

<400> 5

Asp Gly Leu Ser Gln Glu Gln Leu Glu His Arg Glu Arg Ser Leu Gln
1 5 10 15

Thr Leu Arg Asp Ile Gln Arg Met Leu Phe Pro Asp Glu Lys Glu Phe
20 25 30

Thr Gly Ala
35

<210> 6

<211> 15

<212> PRT
<213> Drosophila lgs

<400> 6

Gln	Met	Glu	Trp	Ser	Lys	Ile	Gln	His	Gln	Phe	Phe	Glu	Glu	Arg
1				5					10					15

<210> 7
<211> 15
<212> PRT
<213> Human lgs/bcl9

<400> 7

Gln	Ile	Ala	Trp	Leu	Lys	Leu	Gln	Gln	Glu	Phe	Tyr	Glu	Glu	Lys
1				5					10					15

<210> 8
<211> 9
<212> PRT
<213> Drosophila lgs

<400> 8

Leu	Gln	Gly	Pro	Pro	Pro	Pro	Tyr	His
1				5				

<210> 9
<211> 9
<212> PRT
<213> Human lgs/bcl9

<400> 9

Val	Arg	Gly	Pro	Pro	Pro	Pro	Tyr	Gln
1				5				

<210> 10
<211> 112
<212> PRT
<213> Drosophila lgs

<400> 10

Ser	Ala	Ser	Val	Pro	Ile	Ala	Thr	Gln	Ser	Pro	Asn	Pro	Ser	Ser	Pro
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

1		5						10					15		
Asn	Asn	Leu	Ser	Leu	Pro	Ser	Pro	Arg	Thr	Thr	Ala	Ala	Val	Met	Gly
		20						25					30		
Leu	Pro	Thr	Asn	Ser	Pro	Ser	Met	Asp	Gly	Thr	Gly	Ser	Leu	Ser	Gly
		35					40					45			
Ser	Val	Pro	Gln	Ala	Asn	Thr	Ser	Thr	Val	Gln	Ala	Gly	Thr	Thr	Thr
	50					55					60				
Val	Leu	Ser	Ala	Asn	Lys	Asn	Cys	Phe	Gln	Ala	Asp	Thr	Pro	Ser	Pro
65					70					75					80
Ser	Asn	Gln	Asn	Arg	Ser	Arg	Asn	Thr	Gly	Ser	Ser	Ser	Val	Leu	Thr
				85					90					95	
His	Asn	Leu	Ser	Ser	Asn	Pro	Ser	Thr	Pro	Leu	Ser	His	Leu	Ser	Pro
			100					105					110		

<210> 11
 <211> 111
 <212> PRT
 <213> Human lgs/bcl9

<400> 11

Gly	Pro	Pro	Pro	Pro	Thr	Ala	Ser	Gln	Pro	Ala	Ser	Val	Asn	Ile	Pro
1				5				10					15		
Gly	Ser	Leu	Pro	Ser	Ser	Thr	Pro	Tyr	Thr	Met	Pro	Pro	Glu	Pro	Thr
			20					25					30		
Leu	Ser	Gln	Asn	Pro	Leu	Ser	Ile	Met	Met	Ser	Arg	Met	Ser	Lys	Phe
		35					40					45			
Ala	Met	Pro	Ser	Ser	Thr	Pro	Leu	Tyr	His	Asp	Ala	Ile	Lys	Thr	Val
	50					55					60				

Ala Ser Ser Asp Asp Asp Ser Pro Pro Ala Arg Ser Pro Asn Leu Pro
65 70 75 80

Ser Met Asn Asn Met Pro Gly Met Gly Ile Asn Thr Gln Asn Pro Arg
85 90 95

Ile Ser Gly Pro Asn Pro Val Val Pro Met Pro Thr Leu Ser Pro
100 105 110

<210> 12
<211> 16
<212> PRT
<213> Drosophila lgs

<400> 12

Asn Pro Lys Met Cys Val Ala Gly Gly Pro Asn Gly Pro Pro Gly Phe
1 5 10 15

<210> 13
<211> 16
<212> PRT
<213> Human lgs/bcl9

<400> 13

Asp Ala Ala Leu Cys Lys Pro Gly Gly Pro Gly Gly Pro Asp Ser Phe
1 5 10 15

<210> 14
<211> 4281
<212> DNA
<213> Human lgs/bcl9

<400> 14

atgcattcca gtaaccctaa agtgaggagc tctccatcag gaaacacaca gagtagccct	60
aagtcaaagc aggaggtgat ggtccgtccc cctacagtga tgtccccatc tggaaacccc	120
cagctggatt ccaaattctc caatcagggt aaacaggggg gctcagccag ccaatcccag	180
ccatccccct gtgactccaa gagtgggggc catacccta aagcactccc tggcccaggt	240
gggagcatgg ggctgaagaa tggggctgga aatggtgcca agggcaaggg gaaaaggag	300

cgaagtat	ttt ccgccc	gactc ctttgat	cag agagat	cctg ggactc	caaaa cgatg	actct	360
gacattaa	ag aatgta	attc tgctg	accac ataaag	tccc aggatt	ccca gcacac	acca	420
cactcgat	ga ccccat	caaaa tgctac	agcc cccagg	tctt ctacccc	ctc ccatgg	ccaa	480
actactg	cca cagagc	cccac acctg	ctcag aagact	ccag ccaaag	tgggt gtacgt	gttt	540
tctactg	aga tggcca	aataa agctg	cagaa gctgt	tttga agggcc	caggt tgaaac	tatc	600
gtctctt	ttcc acatcc	cagaa cattt	ctaac aacaag	acag agaga	agcac agcgc	cctct	660
aacacac	aga tatctg	ccct tcgga	atgat ccgaa	acctc tcccac	aaca gcccc	cagct	720
ccggcca	acc aggacc	cagaa ttctt	cccag aatacc	agac tgcag	ccaac tccacc	catt	780
ccggcacc	ag cacc	caagcc tgccg	caccc ccacgt	cccc tggacc	ggga gagtc	cctggg	840
gtagaaa	aca aactg	attcc ttctg	tagga agtcct	gcca gctcc	actcc	actgcccc	900
gatggta	ctg ggccca	actc aactc	ccaac aatagg	gcag tgacc	cctgt ctccc	cagggg	960
agcaata	gct cttcag	caga tccca	aagcc cctccg	cctc caccag	tgtc cagtgg	cgcag	1020
cccccc	acac tgggag	agaa tcccg	atggc ctatct	cagg agcag	ctgga gcacc	ggggag	1080
cgctcct	tac aaactc	tcag agatat	ccag cgcatt	gtt ttctg	atga gaaaga	aatc	1140
acaggag	cac aaagt	ggggg accgc	cagc aatcct	gggg tattag	atgg gcctc	agaaa	1200
aaaccag	aag ggcca	ataca ggccat	gatg gccca	atccc aaagc	cctagg taagg	ggac	1260
gggcccc	gga cagac	gtggg agctc	cattt ggccct	caag gacat	agaga tgtacc	ccttt	1320
tctccag	atg aaatg	gttcc acctt	ctatg aactc	ccagt ctggg	accat aggacc	cgac	1380
caccttg	acc atatg	actcc cgagc	agata gcgtg	ggctga aactg	cagca ggagt	ttttat	1440
gaagaga	aga ggagga	agca ggaaca	agtg gttgt	ccagc agtg	ttccct ccagg	acatg	1500
atgggtc	catc agcac	ggggc tcggg	gagtg gtccg	aggac ccccc	ctcc atacc	cagatg	1560
accctag	tg aaggc	tgggc acctg	ggggg acagag	ccat tttct	gatgg tatca	acatg	1620
ccacatt	ctc tgcccc	cag gggc	atggct cccc	accca acatg	ccagg gagcc	cagatg	1680
cgcctcc	ctg gattt	gcagg catga	tataa tctga	aatgg aaggg	ccgaa tgtccc	caac	1740
cctgcat	cta gaccag	gtct ttctg	gagtc agttg	ggccag atgat	gtgcc aaaa	atccca	1800

gatggtcgaa	attttcctcc	tggccagggc	attttcagcg	gtcctggccg	aggggaacgc	1860
ttcccaaacc	ccaaggatt	gtctgaagag	atgtttcagc	agcagctggc	agagaaacag	1920
ctgggtctcc	ccccagggat	ggccatggaa	ggcatcaggc	ccagcatgga	gatgaacagg	1980
atgattccag	gctcccagcg	ccacatggag	cctgggaata	accccatttt	ccctcgaata	2040
ccagttgagg	gccctctgag	tccttctagg	ggtgactttc	caaaaggaat	tcccccacag	2100
atgggccctg	gtcgggaact	tgagtttggg	atggttccta	gtgggatgaa	gggagatgtc	2160
aatctaaatg	tcaacatggg	atccaactct	cagatgatac	ctcagaagat	gagagaggct	2220
ggggcgggcc	ctgaggagat	gctgaaatta	cgcccagggtg	gctcagacat	gctgcctgct	2280
cagcagaaga	tggtgccact	gccatttggt	gagcaccccc	agcaggagta	tggcatgggc	2340
cccagaccat	tccttcccat	gtctcagggt	ccaggcagca	acagtggctt	gcggaatctc	2400
agagaaccaa	ttgggcccga	ccagaggact	aacagccggc	tcagtcatat	gccaccacta	2460
cctctcaacc	cttccagtaa	ccccaccagc	ctcaacacag	ctcctccagt	tcagcgcggc	2520
ctggggcgga	agcccttgga	tatatctgtg	gcaggcagcc	aggtgcattc	cccaggcatt	2580
aaccctctga	agtctcccac	gatgcaccaa	gtccagtcac	caatgctggg	ctcgccctcg	2640
gggaacctca	agtcccccca	gactccatcg	cagctggcag	gcatgctggc	gggcccagct	2700
gctgctgctt	ccattaagtc	ccccctggt	ttgggggtctg	ctgctgcttc	acctgtccac	2760
ctcaagtctc	catcacttcc	tgccccgtca	cctggatgga	cctcttctcc	aaaacctccc	2820
cttcagagtc	ctgggatccc	tccaaaccat	aaagcacccc	tcaccatggc	ctccccagcc	2880
atgctgggaa	atgtagagtc	aggtggcccc	ccacctccta	cagccagcca	gcctgcctct	2940
gtgaatatcc	ctggaagtct	tcctcttagt	acaccttata	ccatgcctcc	agagccaacc	3000
ctttcccaga	acctactctc	tattatgatg	tctcgaatgt	ccaagtttgc	aatgcccagt	3060
tccaccccgt	tataccatga	tgctatcaag	actgtggcca	gctcagatga	cgactcccct	3120
ccagctcggt	ctcccaactt	gcatcaatg	aataatatgc	caggaatggg	cattaataca	3180
cagaatcctc	gaatttcagg	tccaaacccc	gtggttccga	tgccaaccct	cagcccaatg	3240
ggaatgaccc	agccactttc	tcactccaat	cagatgccct	ctccaaatgc	cgtgggaccc	3300

```

aacatacctc ctcattgggggt cccaatggggg cctgggcttga tgtcacacaaa tcctatcatg 3360
gggcatgggt cccaggagcc accgatggta cctcaaggac ggatgggctt cccccagggc 3420
ttccctccag tacagtctcc cccacagcag gttccattcc ctcacaatgg cccagtgagg 3480
gggcagggca gcttcccagg agggatgggt ttcccaggag aaggccccct tggccgcccc 3540
agcaacctgc cccaaagtcc agcagatgca gcactttgca agcctggagg ccccgggggg 3600
cctgactcct tcaactgtcct ggggaacagc atgccttcgg tgtttacaga cccagatctg 3660
caggagggtca tccgacctgg agccaccgga atacctgagt ttgatctatc ccgcattatt 3720
ccatctgaga agcccagcca gacgctgcaa tatttccctc gaggggaagt tccaggccgt 3780
aaacagcccc agggtcctgg acctggggtt tcacacatgc aggggatgat gggcgaacaa 3840
gccccagaa tgggactagc attacctggc atgggaggtc cagggccagt ggaactccg 3900
gacatccctc ttggtacagc tccatccatg ccaggccaca accccatgag accaccagcc 3960
tttctccaac aaggcatgat gggacctcac catcgatga tgtcaccagc acaatctaca 4020
atgcccggcc agcccaccct gatgagcaat ccagctgctg ccgtgggcat gattcctggc 4080
aaggatcggg ggcctgccgg gctctacacc caccctgggc ctgtgggctc tccaggcatg 4140
atgatgtcca tgcagggcat gatgggaccc caacagaaca tcatgatccc cccacagatg 4200
aggccccggg gcatggctgc tgacgtgggc atgggtggat ttagccaagg acctggcaac 4260
ccaggaaaca tgatgtttta a 4281

```

```

<210> 15
<211> 1426
<212> PRT
<213> Human lgs/bcl9

```

```

<400> 15

```

```

Met His Ser Ser Asn Pro Lys Val Arg Ser Ser Pro Ser Gly Asn Thr
1          5          10          15

```

```

Gln Ser Ser Pro Lys Ser Lys Gln Glu Val Met Val Arg Pro Pro Thr
20          25          30

```

Val	Met	Ser	Pro	Ser	Gly	Asn	Pro	Gln	Leu	Asp	Ser	Lys	Phe	Ser	Asn
		35					40					45			
Gln	Gly	Lys	Gln	Gly	Gly	Ser	Ala	Ser	Gln	Ser	Gln	Pro	Ser	Pro	Cys
	50					55					60				
Asp	Ser	Lys	Ser	Gly	Gly	His	Thr	Pro	Lys	Ala	Leu	Pro	Gly	Pro	Gly
65					70					75					80
Gly	Ser	Met	Gly	Leu	Lys	Asn	Gly	Ala	Gly	Asn	Gly	Ala	Lys	Gly	Lys
				85					90					95	
Gly	Lys	Arg	Glu	Arg	Ser	Ile	Ser	Ala	Asp	Ser	Phe	Asp	Gln	Arg	Asp
			100					105					110		
Pro	Gly	Thr	Pro	Asn	Asp	Asp	Ser	Asp	Ile	Lys	Glu	Cys	Asn	Ser	Ala
		115					120					125			
Asp	His	Ile	Lys	Ser	Gln	Asp	Ser	Gln	His	Thr	Pro	His	Ser	Met	Thr
	130					135					140				
Pro	Ser	Asn	Ala	Thr	Ala	Pro	Arg	Ser	Ser	Thr	Pro	Ser	His	Gly	Gln
145					150					155					160
Thr	Thr	Ala	Thr	Glu	Pro	Thr	Pro	Ala	Gln	Lys	Thr	Pro	Ala	Lys	Val
				165					170					175	
Val	Tyr	Val	Phe	Ser	Thr	Glu	Met	Ala	Asn	Lys	Ala	Ala	Glu	Ala	Val
			180					185					190		
Leu	Lys	Gly	Gln	Val	Glu	Thr	Ile	Val	Ser	Phe	His	Ile	Gln	Asn	Ile
		195					200					205			
Ser	Asn	Asn	Lys	Thr	Glu	Arg	Ser	Thr	Ala	Pro	Leu	Asn	Thr	Gln	Ile
	210					215					220				
Ser	Ala	Leu	Arg	Asn	Asp	Pro	Lys	Pro	Leu	Pro	Gln	Gln	Pro	Pro	Ala
225					230					235					240

Pro	Ala	Asn	Gln	Asp	Gln	Asn	Ser	Ser	Gln	Asn	Thr	Arg	Leu	Gln	Pro	245	250	255
Thr	Pro	Pro	Ile	Pro	Ala	Pro	Ala	Pro	Lys	Pro	Ala	Ala	Pro	Pro	Arg	260	265	270
Pro	Leu	Asp	Arg	Glu	Ser	Pro	Gly	Val	Glu	Asn	Lys	Leu	Ile	Pro	Ser	275	280	285
Val	Gly	Ser	Pro	Ala	Ser	Ser	Thr	Pro	Leu	Pro	Pro	Asp	Gly	Thr	Gly	290	295	300
Pro	Asn	Ser	Thr	Pro	Asn	Asn	Arg	Ala	Val	Thr	Pro	Val	Ser	Gln	Gly	305	310	315
Ser	Asn	Ser	Ser	Ser	Ala	Asp	Pro	Lys	Ala	Pro	Pro	Pro	Pro	Pro	Val	325	330	335
Ser	Ser	Gly	Glu	Pro	Pro	Thr	Leu	Gly	Glu	Asn	Pro	Asp	Gly	Leu	Ser	340	345	350
Gln	Glu	Gln	Leu	Glu	His	Arg	Glu	Arg	Ser	Leu	Gln	Thr	Leu	Arg	Asp	355	360	365
Ile	Gln	Arg	Met	Leu	Phe	Pro	Asp	Glu	Lys	Glu	Phe	Thr	Gly	Ala	Gln	370	375	380
Ser	Gly	Gly	Pro	Gln	Gln	Asn	Pro	Gly	Val	Leu	Asp	Gly	Pro	Gln	Lys	385	390	395
Lys	Pro	Glu	Gly	Pro	Ile	Gln	Ala	Met	Met	Ala	Gln	Ser	Gln	Ser	Leu	405	410	415
Gly	Lys	Gly	Pro	Gly	Pro	Arg	Thr	Asp	Val	Gly	Ala	Pro	Phe	Gly	Pro	420	425	430

Gln Gly His Arg Asp Val Pro Phe Ser Pro Asp Glu Met Val Pro Pro
435 440 445

Ser Met Asn Ser Gln Ser Gly Thr Ile Gly Pro Asp His Leu Asp His
450 455 460

Met Thr Pro Glu Gln Ile Ala Trp Leu Lys Leu Gln Gln Glu Phe Tyr
465 470 475 480

Glu Glu Lys Arg Arg Lys Gln Glu Gln Val Val Val Gln Gln Cys Ser
485 490 495

Leu Gln Asp Met Met Val His Gln His Gly Pro Arg Gly Val Val Arg
500 505 510

Gly Pro Pro Pro Pro Tyr Gln Met Thr Pro Ser Glu Gly Trp Ala Pro
515 520 525

Gly Gly Thr Glu Pro Phe Ser Asp Gly Ile Asn Met Pro His Ser Leu
530 535 540

Pro Pro Arg Gly Met Ala Pro His Pro Asn Met Pro Gly Ser Gln Met
545 550 555 560

Arg Leu Pro Gly Phe Ala Gly Met Ile Asn Ser Glu Met Glu Gly Pro
565 570 575

Asn Val Pro Asn Pro Ala Ser Arg Pro Gly Leu Ser Gly Val Ser Trp
580 585 590

Pro Asp Asp Val Pro Lys Ile Pro Asp Gly Arg Asn Phe Pro Pro Gly
595 600 605

Gln Gly Ile Phe Ser Gly Pro Gly Arg Gly Glu Arg Phe Pro Asn Pro
610 615 620

Gln Gly Leu Ser Glu Glu Met Phe Gln Gln Gln Leu Ala Glu Lys Gln
625 630 635 640

Leu Gly Leu Pro Pro Gly Met Ala Met Glu Gly Ile Arg Pro Ser Met
645 650 655

Glu Met Asn Arg Met Ile Pro Gly Ser Gln Arg His Met Glu Pro Gly
660 665 670

Asn Asn Pro Ile Phe Pro Arg Ile Pro Val Glu Gly Pro Leu Ser Pro
675 680 685

Ser Arg Gly Asp Phe Pro Lys Gly Ile Pro Pro Gln Met Gly Pro Gly
690 695 700

Arg Glu Leu Glu Phe Gly Met Val Pro Ser Gly Met Lys Gly Asp Val
705 710 715 720

Asn Leu Asn Val Asn Met Gly Ser Asn Ser Gln Met Ile Pro Gln Lys
725 730 735

Met Arg Glu Ala Gly Ala Gly Pro Glu Glu Met Leu Lys Leu Arg Pro
740 745 750

Gly Gly Ser Asp Met Leu Pro Ala Gln Gln Lys Met Val Pro Leu Pro
755 760 765

Phe Gly Glu His Pro Gln Gln Glu Tyr Gly Met Gly Pro Arg Pro Phe
770 775 780

Leu Pro Met Ser Gln Gly Pro Gly Ser Asn Ser Gly Leu Arg Asn Leu
785 790 795 800

Arg Glu Pro Ile Gly Pro Asp Gln Arg Thr Asn Ser Arg Leu Ser His
805 810 815

Met Pro Pro Leu Pro Leu Asn Pro Ser Ser Asn Pro Thr Ser Leu Asn
820 825 830

Thr Ala Pro Pro Val Gln Arg Gly Leu Gly Arg Lys Pro Leu Asp Ile
 835 840 845

Ser Val Ala Gly Ser Gln Val His Ser Pro Gly Ile Asn Pro Leu Lys
 850 855 860

Ser Pro Thr Met His Gln Val Gln Ser Pro Met Leu Gly Ser Pro Ser
 865 870 875 880

Gly Asn Leu Lys Ser Pro Gln Thr Pro Ser Gln Leu Ala Gly Met Leu
 885 890 895

Ala Gly Pro Ala Ala Ala Ala Ser Ile Lys Ser Pro Pro Val Leu Gly
 900 905 910

Ser Ala Ala Ala Ser Pro Val His Leu Lys Ser Pro Ser Leu Pro Ala
 915 920 925

Pro Ser Pro Gly Trp Thr Ser Ser Pro Lys Pro Pro Leu Gln Ser Pro
 930 935 940

Gly Ile Pro Pro Asn His Lys Ala Pro Leu Thr Met Ala Ser Pro Ala
 945 950 955 960

Met Leu Gly Asn Val Glu Ser Gly Gly Pro Pro Pro Pro Thr Ala Ser
 965 970 975

Gln Pro Ala Ser Val Asn Ile Pro Gly Ser Leu Pro Ser Ser Thr Pro
 980 985 990

Tyr Thr Met Pro Pro Glu Pro Thr Leu Ser Gln Asn Pro Leu Ser Ile
 995 1000 1005

Met Met Ser Arg Met Ser Lys Phe Ala Met Pro Ser Ser Thr Pro
 1010 1015 1020

Leu Tyr His Asp Ala Ile Lys Thr Val Ala Ser Ser Asp Asp Asp
 1025 1030 1035

Ser	Pro	Pro	Ala	Arg	Ser	Pro	Asn	Leu	Pro	Ser	Met	Asn	Asn	Met
1040						1045					1050			
Pro	Gly	Met	Gly	Ile	Asn	Thr	Gln	Asn	Pro	Arg	Ile	Ser	Gly	Pro
1055						1060					1065			
Asn	Pro	Val	Val	Pro	Met	Pro	Thr	Leu	Ser	Pro	Met	Gly	Met	Thr
1070						1075					1080			
Gln	Pro	Leu	Ser	His	Ser	Asn	Gln	Met	Pro	Ser	Pro	Asn	Ala	Val
1085						1090					1095			
Gly	Pro	Asn	Ile	Pro	Pro	His	Gly	Val	Pro	Met	Gly	Pro	Gly	Leu
1100						1105					1110			
Met	Ser	His	Asn	Pro	Ile	Met	Gly	His	Gly	Ser	Gln	Glu	Pro	Pro
1115						1120					1125			
Met	Val	Pro	Gln	Gly	Arg	Met	Gly	Phe	Pro	Gln	Gly	Phe	Pro	Pro
1130						1135					1140			
Val	Gln	Ser	Pro	Pro	Gln	Gln	Val	Pro	Phe	Pro	His	Asn	Gly	Pro
1145						1150					1155			
Ser	Gly	Gly	Gln	Gly	Ser	Phe	Pro	Gly	Gly	Met	Gly	Phe	Pro	Gly
1160						1165					1170			
Glu	Gly	Pro	Leu	Gly	Arg	Pro	Ser	Asn	Leu	Pro	Gln	Ser	Ser	Ala
1175						1180					1185			
Asp	Ala	Ala	Leu	Cys	Lys	Pro	Gly	Gly	Pro	Gly	Gly	Pro	Asp	Ser
1190						1195					1200			
Phe	Thr	Val	Leu	Gly	Asn	Ser	Met	Pro	Ser	Val	Phe	Thr	Asp	Pro
1205						1210					1215			

Asp	Leu	Gln	Glu	Val	Ile	Arg	Pro	Gly	Ala	Thr	Gly	Ile	Pro	Glu
1220						1225					1230			
Phe	Asp	Leu	Ser	Arg	Ile	Ile	Pro	Ser	Glu	Lys	Pro	Ser	Gln	Thr
1235						1240					1245			
Leu	Gln	Tyr	Phe	Pro	Arg	Gly	Glu	Val	Pro	Gly	Arg	Lys	Gln	Pro
1250						1255					1260			
Gln	Gly	Pro	Gly	Pro	Gly	Phe	Ser	His	Met	Gln	Gly	Met	Met	Gly
1265						1270					1275			
Glu	Gln	Ala	Pro	Arg	Met	Gly	Leu	Ala	Leu	Pro	Gly	Met	Gly	Gly
1280						1285					1290			
Pro	Gly	Pro	Val	Gly	Thr	Pro	Asp	Ile	Pro	Leu	Gly	Thr	Ala	Pro
1295						1300					1305			
Ser	Met	Pro	Gly	His	Asn	Pro	Met	Arg	Pro	Pro	Ala	Phe	Leu	Gln
1310						1315					1320			
Gln	Gly	Met	Met	Gly	Pro	His	His	Arg	Met	Met	Ser	Pro	Ala	Gln
1325						1330					1335			
Ser	Thr	Met	Pro	Gly	Gln	Pro	Thr	Leu	Met	Ser	Asn	Pro	Ala	Ala
1340						1345					1350			
Ala	Val	Gly	Met	Ile	Pro	Gly	Lys	Asp	Arg	Gly	Pro	Ala	Gly	Leu
1355						1360					1365			
Tyr	Thr	His	Pro	Gly	Pro	Val	Gly	Ser	Pro	Gly	Met	Met	Met	Ser
1370						1375					1380			
Met	Gln	Gly	Met	Met	Gly	Pro	Gln	Gln	Asn	Ile	Met	Ile	Pro	Pro
1385						1390					1395			
Gln	Met	Arg	Pro	Arg	Gly	Met	Ala	Ala	Asp	Val	Gly	Met	Gly	Gly
1400						1405					1410			

Phe Ser Gln Gly Pro Gly Asn Pro Gly Asn Met Met Phe
1415 1420 1425

<210> 16
<211> 3948
<212> DNA
<213> Human lgs-1

<400> 16
atggcctgct tcccatcccc tgctgccatc tcctgcaccc ttagggcaca gtgggcatct 60
cgggagctgc tcagcggaca gactaggggtt acccccaccc caggaggaga gaagctccag 120
ggagcccgcc gctgtcccccc gcggtcattg ccccttgccc cagccaagcc aatgcaccca 180
gaaaataaat tgaccaatca tggcaagaca gggaatggcg gggcccaatc tcagcaccag 240
aatgtgaacc aaggaccac ctgcaacgtg ggctcgaagg gcgtgggggc ggggaaccat 300
ggggccaagg ccaaccagat ctgccttagc aactcaagtc tgaagaaccc ccaggcaggg 360
gtgccccctt tcagctcgct caagggcaag gtgaagaggg accggagtgt gtctgtggac 420
tctggagagc agcgagaggc tgggaccca tccctggatt cagaggccaa agaggtggcg 480
ccgcggagta agcggcgctg tgtgctggag cggaagcagc cgtacagtgg ggacgaatgg 540
tgctctggac cggacagtga ggaggacgac aagcccattg gggccacca caaagctgct 600
ttcaaagaag acggctttca ggacaaggca tcacacttct tctccagcac gtacagtcct 660
gaaacctcca ggaggaagct gcccgaagcc ccgaaggctt ccttcctggg gcagcagggc 720
cgagtcattt ggaaacctct ctcgaggag ctccgtgatc aaggtgcaga tgcggcaggt 780
gggccggcct caatcatgtc tccaatcgcg acggtgaatg cgagtggctt gtccaaagag 840
cagctggagc atcgggaacg gtccctccag acgctgcgag acattgagcg actgctgctc 900
cgcagcggag agactgagcc cttcctcaag ggggccccca ggaggagcgg cgggctgaag 960
aaatatgagg aacccttgca gtccatgatt tcacagacac agagcctagg gggccccccg 1020
ctggagcatg aagtgcctgg gcaccccccg ggtggggaca tggggcagca gatgaacatg 1080
atgatacaga ggctgggcca ggacagcctc acgcctgagc aggtggcctg gcgcaagctg 1140

caggaggagt	actacgaaga	gaaacggcgg	aaagaggaac	agattgggct	gcatgggagc	1200
cgtcctctgc	aggacatgat	gggcatgggg	ggcatgatgg	tgagggggcc	cccgccctct	1260
taccacagca	agcctgggga	tcagtggcca	cctggaatgg	gtgcgcagct	gcggggggccc	1320
atggatgttc	aagatcccat	gcagctccgg	ggcggacctc	cctttcctgg	gccccgtttc	1380
ccaggcaacc	agatacaacg	ggtacctggg	tttggggggca	tgcagagtat	gcccattggag	1440
gtgcccattga	atgccatgca	gaggccccgtg	agaccaggca	tgggctggac	cgaagacttg	1500
ccccctatgg	ggggacccag	caattttgcc	cagaacacca	tgccctaccc	aggtggggcag	1560
ggtgaggcgg	agcgattcat	gactccccgg	gtccgtgagg	agctgctgcg	gcaccagctg	1620
ctggagaagc	ggtcgatggg	catgcagcgc	cccctgggca	tggcaggcag	tggcatggga	1680
cagagcatgg	agatggagcg	gatgatgcag	gcgcaccgac	agatggatcc	tgccatgttt	1740
cccgggcaga	tggctggtgg	tgagggcctg	gcggggcactc	ccatggggcat	ggagtttggt	1800
ggaggccggg	gcctcctgag	ccctcccatg	gggcagtctg	ggctgaggga	ggtggaccca	1860
cccatggggc	caggcaacct	caacatgaac	atgaatgtca	acatgaacat	gaacatgaac	1920
ctgaacgtgc	agatgacccc	gcagcagcag	atgctgatgt	cgcagaagat	gcggggccct	1980
ggggacttga	tggggcccca	gggcctcagt	cctgaggaga	tggcccgggt	tcggggcccag	2040
aacagcagtg	gcatggtgcc	cttgccttct	gccaacccgc	caggacctct	caagtcgccc	2100
caggtcctcg	gctcctccct	cagtgtccgt	tcacccactg	gctcgcccag	caggctcaag	2160
tctccttcca	tggcggtgcc	ttctccaggc	tgggttgctt	caccaagac	ggccatgccc	2220
agcccggggg	tctcccagaa	caagcagccg	cctctcaaca	tgaactcttc	caccaccctg	2280
agcaacatgg	aacaggaccc	cacaccttcc	cagaaccccc	tgtcactgat	gatgaccag	2340
atgtccaagt	acgccatgcc	cagctccacc	ccgctctacc	acaatgccat	caagaccatc	2400
gccacctcag	acgacgagct	gctgcccgcg	cggcccctgc	tgcccccccc	accaccaccg	2460
cagggtcccg	ggccagggtgg	ccccgactcc	ctgaatgccc	cctgtggccc	agtgcccagc	2520
tcctcccaga	tgatgccctt	ccccctcgg	ctgcagcagc	cccatgggtgc	catggccccc	2580
actggggggtg	ggggcggggg	gcctggcctg	cagcagcact	accgctcagg	catggccctg	2640

cctccccgagg	acctgccc	aa	ccagccgcca	ggccccatgc	ctccccagca	gcacctgatg	2700
ggcaaagcca	tggctggg	cg	catggg	cgac	gcatacc	cg	2760
gc	atcag	tgc	tgaacg	accc	cgagctg	agc	2820
gaggtgat	cc	ggcccc	acccc	aacgggg	atc		2880
cccgagtt	cg	acttg	tcgag	gatcat	cccc	tctgaga	2940
agc	caagcag	cac	cctccag	tac			3000
ttcccc	caaga	g	cgaga	acca	gcccc	caag	3060
gctcag	cccc	cta	atctg	ca	tctcat	gaac	3120
ctgcaga	aaca	t	gatgg	cgga	gcagact	ccc	3180
tctcgg	cctc	cca	acct	ccc	aggccag	cag	3240
ggcgat	cg	cgctg	ggtg	atacc	gg		3300
ctatgg	cgcc	ggcg	cagc	gc			3360
tgccct	ctgt	gccg	ccag	ac	cttctt	ctgt	3420
ggtcg	cg	ggg	acgttt	acag	ccgca	agc	3480
cagcgg	cagc	tga	aggagg	ctcctg	cccc	aggtgg	3540
aggc	ggagg	ggcccc	gcaag				3600
gccat	ccg	cgctc	agg	ggagc	gctat	gtgccc	3660
gaac	acgag	c	gatg	ctgct	ggtg		3720
ctgtg	ctg	cg	gctgt	gaggt	gcggg	aacac	3780
ctgag	ccatg	gaa	acctg	ac	ggtg	ctgt	3840
gagcaca	aga	aagca	accaa	caa	attct	g	3900
gggggg	ctgc	tggag	catct	ggccag	cccc	gagcaca	3948
agaag	gtttc	tgg	tcact	cc	cagg	attat	
gcgcg	attca	agaa	atccat	ggtg	aaaggt	ttgg	
attc	ct	atga	agaaa	ggagg	ataaa		
gtgat	caagg	agat	ggcag	tcagat	ccgt	gaggtgg	
agc	agag	ccg	aca	ggagg	tggt		
cggt	ctgt	ct	tagag	acag	tcccc	caaga	
tacg	ccct	ca	cagt	ccggt	ccccg	ccg	
ctct	ccc	ggc	gcacg	ctca	gtccg	gtgc	
ttcccc	ccgc	agac	cccc	cga	ggcg	cacc	
ct	ctccc	ggc	gcacg	ctca	gtccg	gtgc	
caag	ctcg	gt	gc	ccccg	cag	ggcg	
ccct	ctg	cg	ccccg	cag	ggcg	ccct	
acc	ctca	agc	tcggt	gtacc	cccc	atacc	
acccg	caag	g	cgcg	ccct	ca	tgccg	
tgccg	cg	gaag					
acttcg	cccc	g	ccca	aggtg	caccc	gtca	
gcccc	gaata	aa	acc	cagtc	actcc	aactt	
gcagg	caaag	ctag	aaaa	ac	tgcg	ctg	
cat	ttg	caa	acaa	aagct	ctt	gt	
tggc	gat	gac					
gata	ctgt	ttt	tgggt	gtg	aa	actgt	
caatt	gcta	act	ac	ta	act	acg	
atct	gt	ga					

<210> 17
 <211> 1115
 <212> PRT
 <213> Human lgs-1

<400> 17

Phe Lys Glu Asp Gly Phe Gln Asp Lys Ala Ser His Phe Phe Ser Ser
1 5 10 15

Thr Tyr Ser Pro Glu Thr Ser Arg Arg Lys Leu Pro Gln Ala Pro Lys
20 25 30

Ala Ser Phe Leu Gly Gln Gln Gly Arg Val Ile Trp Lys Pro Leu Ser
35 40 45

Glu Glu Leu Arg Asp Gln Gly Ala Asp Ala Ala Gly Gly Pro Ala Ser
50 55 60

Ile Met Ser Pro Ile Ala Thr Val Asn Ala Ser Gly Leu Ser Lys Glu
65 70 75 80

Gln Leu Glu His Arg Glu Arg Ser Leu Gln Thr Leu Arg Asp Ile Glu
85 90 95

Arg Leu Leu Leu Arg Ser Gly Glu Thr Glu Pro Phe Leu Lys Gly Ala
100 105 110

Pro Arg Arg Ser Gly Gly Leu Lys Lys Tyr Glu Glu Pro Leu Gln Ser
115 120 125

Met Ile Ser Gln Thr Gln Ser Leu Gly Gly Pro Pro Leu Glu His Glu
130 135 140

Val Pro Gly His Pro Pro Gly Gly Asp Met Gly Gln Gln Met Asn Met
145 150 155 160

Met Ile Gln Arg Leu Gly Gln Asp Ser Leu Thr Pro Glu Gln Val Ala
165 170 175

Trp Arg Lys Leu Gln Glu Glu Tyr Tyr Glu Glu Lys Arg Arg Lys Glu
180 185 190

Glu Gln Ile Gly Leu His Gly Ser Arg Pro Leu Gln Asp Met Met Gly
195 200 205

Met Gly Gly Met Met Val Arg Gly Pro Pro Pro Tyr His Ser Lys
210 215 220

Pro Gly Asp Gln Trp Pro Pro Gly Met Gly Ala Gln Leu Arg Gly Pro
225 230 235 240

Met Asp Val Gln Asp Pro Met Gln Leu Arg Gly Gly Pro Pro Phe Pro
245 250 255

Gly Pro Arg Phe Pro Gly Asn Gln Ile Gln Arg Val Pro Gly Phe Gly
260 265 270

Gly Met Gln Ser Met Pro Met Glu Val Pro Met Asn Ala Met Gln Arg
275 280 285

Pro Val Arg Pro Gly Met Gly Trp Thr Glu Asp Leu Pro Pro Met Gly
290 295 300

Gly Pro Ser Asn Phe Ala Gln Asn Thr Met Pro Tyr Pro Gly Gly Gln
305 310 315 320

Gly Glu Ala Glu Arg Phe Met Thr Pro Arg Val Arg Glu Glu Leu Leu
325 330 335

Arg His Gln Leu Leu Glu Lys Arg Ser Met Gly Met Gln Arg Pro Leu
340 345 350

Gly Met Ala Gly Ser Gly Met Gly Gln Ser Met Glu Met Glu Arg Met
355 360 365

Met Gln Ala His Arg Gln Met Asp Pro Ala Met Phe Pro Gly Gln Met
370 375 380

Ala Gly Gly Glu Gly Leu Ala Gly Thr Pro Met Gly Met Glu Phe Gly
385 390 395 400

Gly Gly Arg Gly Leu Leu Ser Pro Pro Met Gly Gln Ser Gly Leu Arg
405 410 415

Glu Val Asp Pro Pro Met Gly Pro Gly Asn Leu Asn Met Asn Met Asn
420 425 430

Val Asn Met Asn Met Asn Met Asn Leu Asn Val Gln Met Thr Pro Gln
435 440 445

Gln Gln Met Leu Met Ser Gln Lys Met Arg Gly Pro Gly Asp Leu Met
450 455 460

Gly Pro Gln Gly Leu Ser Pro Glu Glu Met Ala Arg Val Arg Ala Gln
465 470 475 480

Asn Ser Ser Gly Met Val Pro Leu Pro Ser Ala Asn Pro Pro Gly Pro
485 490 495

Leu Lys Ser Pro Gln Val Leu Gly Ser Ser Leu Ser Val Arg Ser Pro
500 505 510

Thr Gly Ser Pro Ser Arg Leu Lys Ser Pro Ser Met Ala Val Pro Ser
515 520 525

Pro Gly Trp Val Ala Ser Pro Lys Thr Ala Met Pro Ser Pro Gly Val
530 535 540

Ser Gln Asn Lys Gln Pro Pro Leu Asn Met Asn Ser Ser Thr Thr Leu
545 550 555 560

Ser Asn Met Glu Gln Asp Pro Thr Pro Ser Gln Asn Pro Leu Ser Leu
565 570 575

Met Met Thr Gln Met Ser Lys Tyr Ala Met Pro Ser Ser Thr Pro Leu
580 585 590

Tyr His Asn Ala Ile Lys Thr Ile Ala Thr Ser Asp Asp Glu Leu Leu
595 600 605

Pro Asp Arg Pro Leu Leu Pro Pro Pro Pro Pro Pro Gln Gly Ser Gly
610 615 620

Pro Gly Gly Pro Asp Ser Leu Asn Ala Pro Cys Gly Pro Val Pro Ser
625 630 635 640

Ser Ser Gln Met Met Pro Phe Pro Pro Arg Leu Gln Gln Pro His Gly
645 650 655

Ala Met Ala Pro Thr Gly Gly Gly Gly Gly Gly Pro Gly Leu Gln Gln
660 665 670

His Tyr Pro Ser Gly Met Ala Leu Pro Pro Glu Asp Leu Pro Asn Gln
675 680 685

Pro Pro Gly Pro Met Pro Pro Gln Gln His Leu Met Gly Lys Ala Met
690 695 700

Ala Gly Arg Met Gly Asp Ala Tyr Pro Pro Gly Val Leu Pro Gly Val
705 710 715 720

Ala Ser Val Leu Asn Asp Pro Glu Leu Ser Glu Val Ile Arg Pro Thr
725 730 735

Pro Thr Gly Ile Pro Glu Phe Asp Leu Ser Arg Ile Ile Pro Ser Glu
740 745 750

Lys Pro Ser Ser Thr Leu Gln Tyr Phe Pro Lys Ser Glu Asn Gln Pro
755 760 765

Pro Lys Ala Gln Pro Pro Asn Leu His Leu Met Asn Leu Gln Asn Met
770 775 780

Met Ala Glu Gln Thr Pro Ser Arg Pro Pro Asn Leu Pro Gly Gln Gln
785 790 795 800

Gly Asp Arg Pro Leu Val Val Val Ile Pro Gly Thr Arg Ala Met Ala
805 810 815

Pro Ala Gln Arg Cys Pro Leu Cys Arg Gln Thr Phe Phe Cys Gly Arg
820 825 830

Gly His Val Tyr Ser Arg Lys His Gln Arg Gln Leu Lys Glu Ala Leu
835 840 845

Glu Arg Leu Leu Pro Gln Val Glu Ala Ala Arg Lys Ala Ile Arg Ala
850 855 860

Ala Gln Val Glu Arg Tyr Val Pro Glu His Glu Arg Cys Cys Trp Cys
865 870 875 880

Leu Cys Cys Gly Cys Glu Val Arg Glu His Leu Ser His Gly Asn Leu
885 890 895

Thr Val Leu Tyr Gly Gly Leu Leu Glu His Leu Ala Ser Pro Glu His
900 905 910

Lys Lys Ala Thr Asn Lys Phe Trp Trp Glu Asn Lys Ala Glu Val Gln
915 920 925

Met Lys Glu Lys Phe Leu Val Thr Pro Gln Asp Tyr Ala Arg Phe Lys
930 935 940

Lys Ser Met Val Lys Gly Leu Asp Ser Tyr Glu Glu Lys Glu Asp Lys
945 950 955 960

Val Ile Lys Glu Met Ala Ala Gln Ile Arg Glu Val Glu Gln Ser Arg
965 970 975

Gln Glu Val Val Arg Ser Val Leu Glu Thr Gly Pro Pro Arg Tyr Ala
980 985 990

Leu Thr Val Arg Ser Pro Ala Val Leu Ser Arg Arg Thr Leu Lys Ser
995 1000 1005

Gly Ala Phe Pro Pro Gln Thr Pro Glu Ala His Pro Gln Ala Arg
1010 1015 1020

Cys Leu Cys Ala Pro Arg Arg Gly Ala Leu Lys Pro Glu Pro Pro
1025 1030 1035

Gly Arg Thr Leu Lys Leu Gly Val Pro Pro His Thr Thr Arg Lys
1040 1045 1050

Ala Arg Pro His Ala Ala Lys Thr Ser Pro Arg Pro Arg Cys Thr
1055 1060 1065

Arg Gln Ala Pro Asn Lys Thr Gln Ser Leu Gln Leu Ala Gly Lys
1070 1075 1080

Ala Arg Lys Thr Ala Leu His Leu Gln Thr Lys Ala Leu Val Gly
1085 1090 1095

Asp Asp Asp Thr Val Leu Gly Val Lys Leu Ser Ile Ala Asn Tyr
1100 1105 1110

Asp Leu
1115

<210> 18
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> T7 Promoter containing dsRNA-lgs-R1

<220>
<221> misc_structure
<222> (1)..(49)
<223> T7 Promoter containing dsRNA-lgs-R1

<400> 18
taatacgact cactataggg agaccacttc catgctcatt tcgtcatta

49

<210> 19
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> dsRNA-lgs-F1

<220>
<221> misc_structure
<222> (1)..(48)
<223> dsRNA-lgs-F1

<400> 19
taatacgact cactataggg agaccactag gatctctcga caacaatg

48

<210> 20
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> F Primer

<220>
<221> misc_structure
<222> (1)..(49)
<223> F Primer

<400> 20
taatacgact cactataggg agaccacaca agaccaagtg gacgatatg

49

<210> 21
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> R Primer

<220>

<221> misc_structure
<222> (1)..(48)
<223> R Primer

<400> 21
taatacgact cactataggg agaccacaat ttgcaagcaa tctgtgac

48

<210> 22
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> T7 Promoter

<220>
<221> misc_structure
<222> (1)..(27)
<223> T7 Promoter

<400> 22
taatacgact cactataggg agaccac

27

<210> 23
<211> 1464
<212> PRT
<213> Drosophila lgs

<400> 23

Met Pro Arg Ser Pro Thr Gln Gln Gln Pro Gln Pro Asn Ser Asp Ala
1 5 10 15

Ser Ser Thr Ser Ala Ser Gly Ser Asn Pro Gly Ala Ala Ile Gly Asn
20 25 30

Gly Asp Ser Ala Ala Ser Arg Ser Ser Pro Lys Thr Leu Asn Ser Glu
35 40 45

Pro Phe Ser Thr Leu Ser Pro Asp Gln Ile Lys Leu Thr Pro Glu Glu
50 55 60

Gly Thr Glu Lys Ser Gly Leu Ser Thr Ser Asp Lys Ala Ala Thr Gly

65					70					75					80
Gly	Ala	Pro	Gly	Ser	Gly	Asn	Asn	Leu	Pro	Glu	Gly	Gln	Thr	Met	Leu
				85					90					95	
Arg	Gln	Asn	Ser	Thr	Ser	Thr	Ile	Asn	Ser	Cys	Leu	Val	Ala	Ser	Pro
			100					105					110		
Gln	Asn	Ser	Ser	Glu	His	Ser	Asn	Ser	Ser	Asn	Val	Ser	Ala	Thr	Val
		115					120					125			
Gly	Leu	Thr	Gln	Met	Val	Asp	Cys	Asp	Glu	Gln	Ser	Lys	Lys	Asn	Lys
	130					135					140				
Cys	Ser	Val	Lys	Asp	Glu	Glu	Ala	Glu	Ile	Ser	Ser	Asn	Lys	Ala	Lys
145					150					155					160
Gly	Gln	Ala	Ala	Gly	Gly	Gly	Cys	Glu	Thr	Gly	Ser	Thr	Ser	Ser	Leu
				165					170					175	
Thr	Val	Lys	Glu	Glu	Pro	Thr	Asp	Val	Leu	Gly	Ser	Leu	Val	Asn	Met
			180					185					190		
Lys	Lys	Glu	Glu	Arg	Glu	Asn	His	Ser	Pro	Thr	Met	Ser	Pro	Val	Gly
		195					200					205			
Phe	Gly	Ser	Ile	Gly	Asn	Ala	Gln	Asp	Asn	Ser	Ala	Thr	Pro	Val	Lys
	210					215					220				
Ile	Glu	Arg	Ile	Ser	Asn	Asp	Ser	Thr	Thr	Glu	Lys	Lys	Gly	Ser	Ser
225					230					235					240
Leu	Thr	Met	Asn	Asn	Asp	Glu	Met	Ser	Met	Glu	Gly	Cys	Asn	Gln	Leu
				245					250					255	
Asn	Pro	Asp	Phe	Ile	Asn	Glu	Ser	Leu	Asn	Asn	Pro	Ala	Ile	Ser	Ser
			260					265					270		

Ile Leu Val Ser Gly Val Gly Pro Ile Pro Gly Ile Gly Val Gly Ala
275 280 285

Gly Thr Gly Asn Leu Leu Thr Ala Asn Ala Asn Gly Ile Ser Ser Gly
290 295 300

Ser Ser Asn Cys Leu Asp Tyr Met Gln Gln Gln Asn His Ile Phe Val
305 310 315 320

Phe Ser Thr Gln Leu Ala Asn Lys Gly Ala Glu Ser Val Leu Ser Gly
325 330 335

Gln Phe Gln Thr Ile Ile Ala Tyr His Cys Thr Gln Pro Ala Thr Lys
340 345 350

Ser Phe Leu Glu Asp Phe Phe Met Lys Asn Pro Leu Lys Ile Asn Lys
355 360 365

Leu Gln Arg His Asn Ser Val Gly Met Pro Trp Ile Gly Met Gly Gln
370 375 380

Val Gly Leu Thr Pro Pro Asn Pro Val Ala Lys Ile Thr Gln Gln Gln
385 390 395 400

Pro His Thr Lys Thr Val Gly Leu Leu Lys Pro Gln Phe Asn Gln His
405 410 415

Glu Asn Ser Lys Arg Ser Thr Val Ser Ala Pro Ser Asn Ser Phe Val
420 425 430

Asp Gln Ser Asp Pro Met Gly Asn Glu Thr Glu Leu Met Cys Trp Glu
435 440 445

Gly Gly Ser Ser Asn Thr Ser Arg Ser Gly Gln Asn Ser Arg Asn His
450 455 460

Val Asp Ser Ile Ser Thr Ser Ser Glu Ser Gln Ala Ile Lys Ile Leu

465					470					475				480	
Glu	Ala	Ala	Gly	Val	Asp	Leu	Gly	Gln	Val	Thr	Lys	Gly	Ser	Asp	Pro
			485						490					495	
Gly	Leu	Thr	Thr	Glu	Asn	Asn	Ile	Val	Ser	Leu	Gln	Gly	Val	Lys	Val
			500					505					510		
Pro	Asp	Glu	Asn	Leu	Thr	Pro	Gln	Gln	Arg	Gln	His	Arg	Glu	Glu	Gln
		515					520					525			
Leu	Ala	Lys	Ile	Lys	Lys	Met	Asn	Gln	Phe	Leu	Phe	Pro	Glu	Asn	Glu
	530					535					540				
Asn	Ser	Val	Gly	Ala	Asn	Val	Ser	Ser	Gln	Ile	Thr	Lys	Ile	Pro	Gly
545					550					555					560
Asp	Leu	Met	Met	Gly	Met	Ser	Gly	Gly	Gly	Gly	Gly	Ser	Ile	Ile	Asn
				565					570					575	
Pro	Thr	Met	Arg	Gln	Leu	His	Met	Pro	Gly	Asn	Ala	Lys	Ser	Glu	Leu
			580					585					590		
Leu	Ser	Ala	Thr	Ser	Ser	Gly	Leu	Ser	Glu	Asp	Val	Met	His	Pro	Gly
		595					600					605			
Asp	Val	Ile	Ser	Asp	Met	Gly	Ala	Val	Ile	Gly	Cys	Asn	Asn	Asn	Gln
	610					615					620				
Lys	Thr	Ser	Val	Gln	Cys	Gly	Ser	Gly	Val	Gly	Val	Val	Thr	Gly	Thr
625					630					635					640
Thr	Ala	Ala	Gly	Val	Asn	Val	Asn	Met	His	Cys	Ser	Ser	Ser	Gly	Ala
			645					650						655	
Pro	Asn	Gly	Asn	Met	Met	Gly	Ser	Ser	Thr	Asp	Met	Leu	Ala	Ser	Phe
			660					665					670		

Gly Asn Thr Ser Cys Asn Val Ile Gly Thr Ala Pro Asp Met Ser Lys
675 680 685

Glu Val Leu Asn Gln Asp Ser Arg Thr His Ser His Gln Gly Gly Val
690 695 700

Ala Gln Met Glu Trp Ser Lys Ile Gln His Gln Phe Phe Glu Glu Arg
705 710 715 720

Leu Lys Gly Gly Lys Pro Arg Gln Val Thr Gly Thr Val Val Pro Gln
725 730 735

Gln Gln Thr Pro Ser Gly Ser Gly Gly Asn Ser Leu Asn Asn Gln Val
740 745 750

Arg Pro Leu Gln Gly Pro Pro Pro Pro Tyr His Ser Ile Gln Arg Ser
755 760 765

Ala Ser Val Pro Ile Ala Thr Gln Ser Pro Asn Pro Ser Ser Pro Asn
770 775 780

Asn Leu Ser Leu Pro Ser Pro Arg Thr Thr Ala Ala Val Met Gly Leu
785 790 795 800

Pro Thr Asn Ser Pro Ser Met Asp Gly Thr Gly Ser Leu Ser Gly Ser
805 810 815

Val Pro Gln Ala Asn Thr Ser Thr Val Gln Ala Gly Thr Thr Thr Val
820 825 830

Leu Ser Ala Asn Lys Asn Cys Phe Gln Ala Asp Thr Pro Ser Pro Ser
835 840 845

Asn Gln Asn Arg Ser Arg Asn Thr Gly Ser Ser Ser Val Leu Thr His
850 855 860

Asn Leu Ser Ser Asn Pro Ser Thr Pro Leu Ser His Leu Ser Pro Lys

865		870		875		880
Glu Phe Glu Ser Phe Gly Gln Ser Ser Ala Gly Asp Asn Met Lys Ser						
		885		890		895
Arg Arg Pro Ser Pro Gln Gly Gln Arg Ser Pro Val Asn Ser Leu Ile						
		900		905		910
Glu Ala Asn Lys Asp Val Arg Phe Ala Ala Ser Ser Pro Gly Phe Asn						
		915		920		925
Pro His Pro His Met Gln Ser Asn Ser Asn Ser Ala Leu Asn Ala Tyr						
		930		935		940
Lys Met Gly Ser Thr Asn Ile Gln Met Glu Arg Gln Ala Ser Ala Gln						
		945		950		955
						960
Gly Gly Ser Val Gln Phe Ser Arg Arg Ser Asp Asn Ile Pro Leu Asn						
		965		970		975
Pro Asn Ser Gly Asn Arg Pro Pro Pro Asn Lys Met Thr Gln Asn Phe						
		980		985		990
Asp Pro Ile Ser Ser Leu Ala Gln Met Ser Gln Gln Leu Thr Ser Cys						
		995		1000		1005
Val Ser Ser Met Gly Ser Pro Ala Gly Thr Gly Gly Met Thr Met						
		1010		1015		1020
Met Gly Gly Pro Gly Pro Ser Asp Ile Asn Ile Glu His Gly Ile						
		1025		1030		1035
Ile Ser Gly Leu Asp Gly Ser Gly Ile Asp Thr Ile Asn Gln Asn						
		1040		1045		1050
Asn Cys His Ser Met Asn Val Val Met Asn Ser Met Gly Pro Arg						
		1055		1060		1065

Met Leu Asn Pro Lys Met Cys Val Ala Gly Gly Pro Asn Gly Pro
1070 1075 1080

Pro Gly Phe Asn Pro Asn Ser Pro Asn Gly Gly Leu Arg Glu Asn
1085 1090 1095

Ser Ile Gly Ser Gly Cys Gly Ser Ala Asn Ser Ser Asn Phe Gln
1100 1105 1110

Gly Val Val Pro Pro Gly Ala Arg Met Met Gly Arg Met Pro Val
1115 1120 1125

Asn Phe Gly Ser Asn Phe Asn Pro Asn Ile Gln Val Lys Ala Ser
1130 1135 1140

Thr Pro Asn Thr Ile Gln Tyr Met Pro Val Arg Ala Gln Asn Ala
1145 1150 1155

Asn Asn Asn Asn Asn Asn Gly Ala Asn Asn Val Arg Met Pro Pro
1160 1165 1170

Ser Leu Glu Phe Leu Gln Arg Tyr Ala Asn Pro Gln Met Gly Ala
1175 1180 1185

Val Gly Asn Gly Ser Pro Ile Cys Pro Pro Ser Ala Ser Asp Gly
1190 1195 1200

Thr Pro Gly Met Pro Gly Leu Met Ala Gly Pro Gly Ala Gly Gly
1205 1210 1215

Met Leu Met Asn Ser Ser Gly Glu Gln His Gln Asn Lys Ile Thr
1220 1225 1230

Asn Asn Pro Gly Ala Ser Asn Gly Ile Asn Phe Phe Gln Asn Cys
1235 1240 1245

Asn Gln Met Ser Ile Val Asp Glu Glu Gly Gly Leu Pro Gly His

1250						1255					1260			
Asp	Gly	Ser	Met	Asn	Ile	Gly	Gln	Pro	Ser	Met	Ile	Arg	Gly	Met
1265						1270					1275			
Arg	Pro	His	Ala	Met	Arg	Pro	Asn	Val	Met	Gly	Ala	Arg	Met	Pro
1280						1285					1290			
Pro	Val	Asn	Arg	Gln	Ile	Gln	Phe	Ala	Gln	Ser	Ser	Asp	Gly	Ile
1295						1300					1305			
Asp	Cys	Val	Gly	Asp	Pro	Ser	Ser	Phe	Phe	Thr	Asn	Ala	Ser	Cys
1310						1315					1320			
Asn	Ser	Ala	Gly	Pro	His	Met	Phe	Gly	Ser	Ala	Gln	Gln	Ala	Asn
1325						1330					1335			
Gln	Pro	Lys	Thr	Gln	His	Ile	Lys	Asn	Ile	Pro	Ser	Gly	Met	Cys
1340						1345					1350			
Gln	Asn	Gln	Ser	Gly	Leu	Ala	Val	Ala	Gln	Gly	Gln	Ile	Gln	Leu
1355						1360					1365			
His	Gly	Gln	Gly	His	Ala	Gln	Gly	Gln	Ser	Leu	Ile	Gly	Pro	Thr
1370						1375					1380			
Asn	Asn	Asn	Leu	Met	Ser	Thr	Ala	Gly	Ser	Val	Ser	Ala	Thr	Asn
1385						1390					1395			
Gly	Val	Ser	Gly	Ile	Asn	Phe	Val	Gly	Pro	Ser	Ser	Thr	Asp	Leu
1400						1405					1410			
Lys	Tyr	Ala	Gln	Gln	Tyr	His	Ser	Phe	Gln	Gln	Gln	Leu	Tyr	Ala
1415						1420					1425			
Thr	Asn	Thr	Arg	Ser	Gln	Gln	Gln	Gln	His	Met	His	Gln	Gln	His
1430						1435					1440			

Gln Ser Asn Met Ile Thr Met Pro Pro Asn Leu Ser Pro Asn Pro
 1445 1450 1455

Thr Phe Phe Val Asn Lys
 1460

<210> 24
 <211> 28
 <212> PRT
 <213> Drosophila lgs

<220>
 <221> misc_feature
 <222> (1)..(2)
 <223> Xaa can be any naturally occurring amino acid

<220>
 <221> misc_feature
 <222> (7)..(8)
 <223> Xaa can be any naturally occurring amino acid

<220>
 <221> misc_feature
 <222> (12)..(12)
 <223> Xaa can be any naturally occurring amino acid

<220>
 <221> misc_feature
 <222> (15)..(15)
 <223> Xaa can be any naturally occurring amino acid

<220>
 <221> misc_feature
 <222> (18)..(18)
 <223> Xaa can be any naturally occurring amino acid

<220>
 <221> misc_feature
 <222> (21)..(22)
 <223> Xaa can be any naturally occurring amino acid

<220>
 <221> misc_feature
 <222> (25)..(27)
 <223> Xaa can be any naturally occurring amino acid

<400> 24

Xaa	Xaa	Val	Phe	Ser	Thr	Xaa	Xaa	Ala	Asn	Lys	Xaa	Ala	Glu	Xaa	Val
1				5					10					15	

Leu	Xaa	Gly	Gln	Xaa	Xaa	Thr	Ile	Xaa	Xaa	Xaa	His
			20					25			

<210> 25

<211> 35

<212> PRT

<213> Drosophila lgs

<220>

<221> misc_feature

<222> (1)..(2)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> misc_feature

<222> (4)..(6)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> misc_feature

<222> (8)..(9)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> misc_feature

<222> (13)..(14)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> misc_feature

<222> (16)..(24)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> misc_feature

<222> (28)..(33)

<223> Xaa can be any naturally occurring amino acid

<400> 25

Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Gln	Xaa	Xaa	His	Arg	Glu	Xaa	Xaa	Leu	Xaa
1				5					10					15	

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Phe Pro Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Gly Ala
35